

Complete Genome Sequencing of a Novel *Gloeobacter* Species from a Waterfall Cave in Mexico

Jimmy H. Saw ^{1,*}, Tanai Cardona ², and Gustavo Montejano³

¹Department of Biological Sciences, The George Washington University, District of Columbia, USA

²Department of Life Sciences, Imperial College London, United Kingdom

³Facultad de Ciencias, Laboratorio de Ficología, National Autonomous University of Mexico, Ciudad de México, Mexico

*Corresponding author: E-mail: jsaw@gwu.edu.

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Data deposition: The complete genome sequence of *Gloeobacter morelensis* has been deposited at GenBank under accessions accession numbers CP063845–CP063847. This project has been deposited at NCBI under the Bioproject accession number PRJNA671611.

Abstract

Only two complete genomes of the cyanobacterial genus *Gloeobacter* from two very different regions of the world currently exist. Here, we present the complete genome sequence of a third member of the genus isolated from a waterfall cave in Mexico. Analysis of the average nucleotide identities (ANIs) between published *Gloeobacter* genomes revealed that the complete genome of this new member is only 92.7% similar to *Gloeobacter violaceus* and therefore we determined it to be a new species. We propose to name this new species *Gloeobacter morelensis* after the location in Mexico where it was isolated. The complete genome consists of one circular chromosome (4,921,229 bp), one linear plasmid (172,328 bp), and one circular plasmid (8,839 bp). Its genome is the largest of all completely sequenced genomes of *Gloeobacter* species. Pangenomic comparisons revealed that *G. morelensis* encodes 759 genes not shared with other *Gloeobacter* species. Despite being more closely related to *G. violaceus*, it features an extremely divergent *psbA* gene encoding an atypical D1 core subunit of Photosystem II previously only found within the genome of *Gloeobacter kilauensis*. In addition, we detected evidence of concerted evolution of *psbA* genes encoding identical D1 in all three *Gloeobacter* genomes, a characteristic that seems widespread in cyanobacteria and may therefore be traced back to their last common ancestor.

Key words: *Gloeobacter*, oxygenic photosynthesis, cave, waterfall, evolution, photosystem.

Significance

Cyanobacteria of the genus *Gloeobacter* display ancestral features thought to be present during the early stages of the evolution of oxygenic photosynthesis, a process that led to the accumulation of oxygen in the Earth's atmosphere. Despite their importance to understanding the origin and evolution of cyanobacteria, only two complete genomes of *Gloeobacter* have been sequenced so far. Additional complete genomes of *Gloeobacter* are needed to better understand ancestral and derived features of oxygenic photosynthesis in this group of thylakoid-less cyanobacteria. The complete genome of the third member of the cyanobacterial genus *Gloeobacter* contributes to filling the knowledge gap on how oxygenic cyanobacteria first arose and diversified on the early Earth.

Introduction

Cyanobacteria of the genus *Gloeobacter* are the earliest-branching members of cyanobacteria capable of oxygenic photosynthesis, a process that led to the accumulation of oxygen

gas in the Earth's atmosphere and paved the way for aerobic organisms to diversify. Members of the genus *Gloeobacter* lack thylakoid membranes typically associated with cyanobacteria and plastids, a feature conserved in all other oxygenic

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phototrophs (Rippka et al. 1974). They are widely distributed but poorly represented in terms of genomic sequences and cultivated species. Only two members of the genus *Gloeobacter* have been cultivated thus far with their complete genomes sequenced (Nakamura et al. 2003; Saw et al. 2013). In 2020, a distantly related sister taxon to *Gloeobacter* was reported from metagenomes of microbial mats in an Antarctic lake and was named *Aurora vandensis* (Grettenberger et al. 2020). Recently, a novel strain closely related to *A. vandensis* that also lacks thylakoids was isolated from a hornwort and named *Anthocerotibacter panamensis*. Its complete genome was reported recently (Rahmatpour et al. 2021).

Photosystem II is a highly conserved enzymatic complex of cyanobacteria that catalyzes the light-driven oxidation of water to molecular oxygen. Therefore, understanding the evolution of Photosystem II is essential to pinpoint the origin of oxygenic photosynthesis (Rutherford and Faller 2003). Given the phylogenetic position of *Gloeobacter* in the cyanobacteria tree of life, there is interest in deciphering whether this clade retains ancestral photosystem traits that could provide insight into how oxygenic photosynthesis first emerged.

However, although the genome content of *Gloeobacteriales* appeared to show a slightly decreased number of identifiable accessory photosystem subunits (Nakamura et al. 2003; Saw et al. 2013; Rahmatpour et al. 2021), measurements of oxygen evolution activity in *Gloeobacter violaceus* PCC 7421 revealed no functional differences to model organisms (Koyama et al. 2008). The genome of *Gloeobacter kilaueensis* JS1, on the other hand, revealed an additional Photosystem II subunit with atypical characteristics previously undetected in the closely related *G. violaceus* genome. This subunit was the least conserved version of any catalytic subunit (D1) of Photosystem II described to date in cyanobacteria and photosynthetic eukaryotes (Cardona et al. 2015). It was denoted Group 0 as it remained a singularity, and its phylogenetic position was interpreted to suggest it originated from an ancient gene duplication event of a Photosystem II D1 subunit (Cardona et al. 2015), antedating the last common ancestor of cyanobacteria by well over half a billion years (Cardona et al. 2019).

Here, we present the complete genome sequence of an additional member of the *Gloeobacter*. Comparisons of complete genomes and pangenomes revealed that this member is a different species closely related to *G. violaceus*. Surprisingly, the genome of this new *Gloeobacter* has a gene encoding the atypical Group 0 D1 that is not found in the genome of the more closely related *G. violaceus* but is found in the genome of the distantly related *G. kilaueensis*. Very few complete genomes of *Gloeobacter* and related species exist and the addition of this novel *Gloeobacter* species is therefore crucial to further bridge the knowledge gap that exists in our understanding of how oxygenic photosynthesis arose on Earth and

how cyanobacteria first acquired this important biological function.

Results and Discussion

Genome Assembly, Annotation, and Comparison with Other *Gloeobacter* spp

A combined total of 2,157,121,864 clean and trimmed high-quality bases were obtained from both Illumina and Nanopore sequence reads. A hybrid assembly using both short-read Illumina and long-read Nanopore sequences produced a genome assembly without any gaps (table 1). The genome assembly performed using Unicycler (Wick et al. 2017) resulted in three contigs and the analysis of Unicycler genome assembly paths using the Bandage tool (Wick et al. 2015) indicated a circular chromosome of 4,921,229 bp, a linear plasmid of 172,328 bp, and a circular plasmid of 8,839 bp (supplementary fig. S1, Supplementary Material online). CheckM and miccomplete analyses revealed high genome completeness (>99% and 100% complete, respectively) and low level of contamination (<1%) (supplementary table S1, Supplementary Material online). The level of completeness reported by CheckM and miccomplete tools may not accurately reflect the actual completeness due to the use of so-called universal single-copy genetic markers. These marker gene sets vary between divergent organisms and low completeness scores may be reported even for highly complete genomes. To obtain an independent estimate of the quality of genome assembly, we used BUSCO to assess genome completeness and marker gene contents of closely related *Gloeobacter* and associated lineages. This tool was originally designed for eukaryotic genomes but has been updated to assess marker genes in prokaryotes as well (Manni et al. 2021). BUSCO analysis using universal and cyanobacteria marker gene sets revealed similar levels of genome completeness and marker gene presence in the genome sequences of three *Gloeobacter* species (supplementary fig. S3, Supplementary Material online).

A total of 4,755 coding sequences (CDS) were identified by the NCBI PGAP automatic annotation pipeline (v4.6) (table 1). Three CRISPR (Clustered Regularly Interspaced Palindromic Repeats) regions were identified in the circular chromosome. The genome of this newly sequenced *Gloeobacter* is the largest among the three *Gloeobacter* with complete genomic sequences: 4.92 Mbp for the circular chromosome compared with 4.72 Mbp for *G. kilaueensis* and 4.66 Mbp for *G. violaceus* PCC 7421. PyANI calculation using ANIb (Pritchard et al. 2016) revealed that *Gloeobacter violaceus* PCC 7421 and the newly sequenced *Gloeobacter* share only 92.6% average nucleotide identity (ANI) despite having 99.93% 16S rRNA gene sequence identity. This value is below the threshold value for delineating species (Jain et al. 2018). Genome-to-genome distance calculator (Meier-Kolthoff et al.

Table 1

General Features of the Genome

Feature	Chromosome (Circular)	Plasmid 1 (Linear)	Plasmid 2 (Circular)
Length (bp)	4,921,229	172,328	8,839
GC content (%)	61.86	58.85	59.07
CDS	4,569	177	9
Pseudogenes	107	1	1
CRISPR arrays	3	0	0
rRNA (5S, 16S, 23S)	1, 1, 1	0, 0, 0	0, 0, 0
tRNA	44	0	0

2013) revealed a value of 49.4% between *G. violaceus* PCC 7421 and the new *Gloeobacter* genome, which is well below the 70% cutoff value for delineating species based on in silico DNA–DNA hybridization (Wayne 1988; Stackebrandt and Goebel 1994). The new *Gloeobacter* genome has 98.7% 16S rRNA gene sequence identity and ANI of 75.73% to *G. kilaueensis*. Based on these metrics, this newly sequenced genome of *Gloeobacter* likely belongs to a new species and we propose to name it *Gloeobacter morelensis* based on the origin of the biofilm materials (Morelos, Mexico) from which this cyanobacterium was isolated. The genus and species names of *G. violaceus*, the first cultivated member of this cyanobacterial lineage, was first published in 1974 (Rippka et al. 1974) and validated in 2013 (Mareš et al. 2013). Here, we have decided to preserve the genus name of the lineage. Formal description of the species is beyond the scope of this study as we have not yet deposited the pure culture to a culture collection agency, but we plan to further characterize this novel species in greater detail in the near future.

Phylogenomic Analysis

PhyloPhlAn (v3.0.51) (Asnicar et al. 2020) identified 395 unique single-copy genes in 159 cyanobacterial genomes (including the genome of *G. morelensis*) with species designations from the NCBI database. This workflow aligned, trimmed, and concatenated the single-copy genes and the concatenated alignment was used as an input to run IQ-TREE (v2.0.3) (Minh et al. 2020) with the best-fit model predicted by the tool. The resulting maximum likelihood phylogenomic tree was rooted with sequences from Melainabacteria, Sericytochromatia, and Margulisbacteria (Soo et al. 2019). The phylogenomic tree shows two deeply branching and distinct sister clades of oxyphotobacteria, one consisting of *G. violaceus*, *G. kilaueensis*, *Gloeobacter* SpSt-379 (from a metagenome bin), and *G. morelensis* and the other consisting of *A. panamensis* and *A. vandensis* isolates LV9 and MP9P1 with 100% ultrarapid bootstrap support (fig. 1A; supplementary fig. S2, Supplementary Material online). *Gloeobacter morelensis* is the sister lineage of *G. violaceus* PCC 7421 in the phylogenomic tree. The

topology of the tree is similar to the tree obtained by Rahmatpour et al. (2021).

Pangenomic Analysis

To identify unique and shared genes among the four *Gloeobacter* species and two sister taxa, we used Anvi'o (Eren et al. 2021) to perform a pangenomic comparison of their genomes. The analysis revealed that the genome of *G. morelensis* encodes 729 unique gene clusters (759 unique genes) not shared with other genomes (fig. 1B; supplementary table S2, Supplementary Material online). *Aurora vandensis* LV9 and *A. panamensis* form a distinct clade diverged from the *Gloeobacter* clade based on ANI values. They share very low ANI values with *Gloeobacter* species: between 69.93% and 70.42% (fig. 1). Core gene clusters shared between genomes included in this analysis is 580. *Gloeobacter morelensis* and *G. violaceus* PCC 7421 share 798 unique gene clusters (1,717 genes total) between them (supplementary table S2, Supplementary Material online).

Photosystem II D1 Evolution

The unrooted phylogeny of D1 is shown in figure 2 and is similar to those presented by previous authors (Sheridan et al. 2020). Photosystem II adapts to changing environments by swapping D1 subunits to variant forms better tuned to new conditions. These sequence variants can range from just a few amino acid changes to forms exhibiting >40% amino acid substitutions when compared with the well characterized standard D1 (Group 4, G4, blue). The more divergent forms, like for example, “ChIF” (Group 1, G1, purple), enables Photosystem II to acquire new functions beyond oxygen evolution, such as chlorophyll *f* synthesis in the far-red light photoacclimation response (FaRLiP) (Ho et al. 2016; Trinugroho et al. 2020). In the same response, another variant D1 (olive), uses chlorophyll *f* in a Photosystem II complex to enable oxygen evolution under far-red light conditions (Gan et al. 2014; Nürnberg et al. 2018). Nonetheless, all known cyanobacteria capable of oxygenic photosynthesis retain at least one, but often several standard D1, which is the main catalytic form of D1 used in oxygen evolution activity. The branches designated G0 (gray) represents the most divergent D1 amino acid

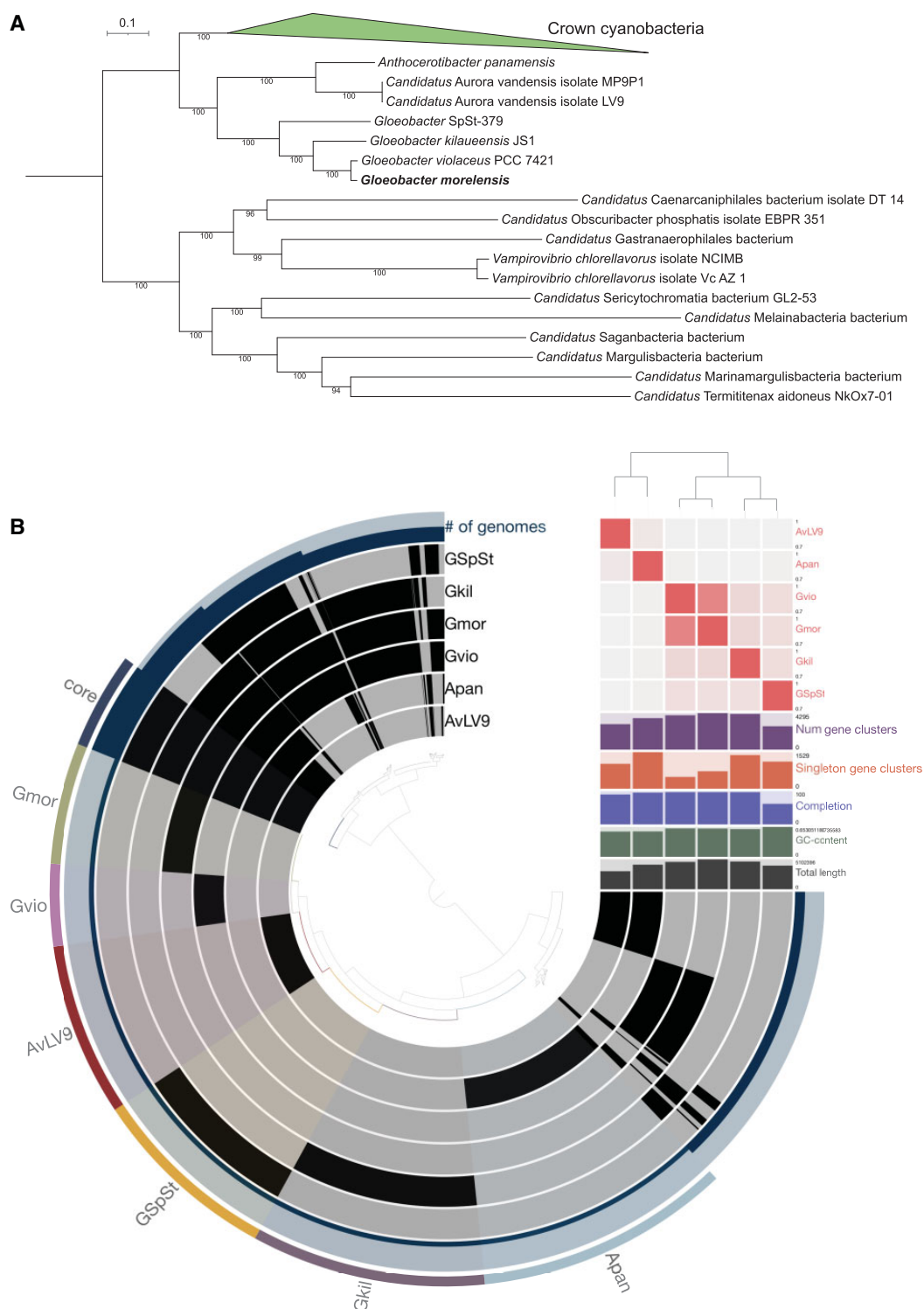


Fig. 1.—(A) Phylogenomic tree displaying placement of *Gloeobacter morelensis* with closely related lineages. Only the names of *Gloeobacter*-associated lineages and members of the outgroup are shown. Full tree with names of all lineages can be found in [supplementary figure S1, Supplementary Material online](#). (B) Pangenomic comparison of three complete genomes and a draft genome of *Gloeobacter* species using the Anvi'o tool. Core gene clusters shared by all species are highlighted and labeled as "core" and gene clusters present in each species are highlighted and labeled as "Gmor," "Gvio," "AvLV9," "GSpSt," "Gkil," and "Apan" to represent *G. morelensis*, *G. violaceus*, *A. vandensis* LV9, *G. SpSt-379*, *G. kilaeensis*, and *A. panamensis*, respectively. ANIs between them are shown as a heatmap in red near the top right quadrant of the figure. Placement of the genomes is based on ANI similarities as predicted by the PyANI tool.

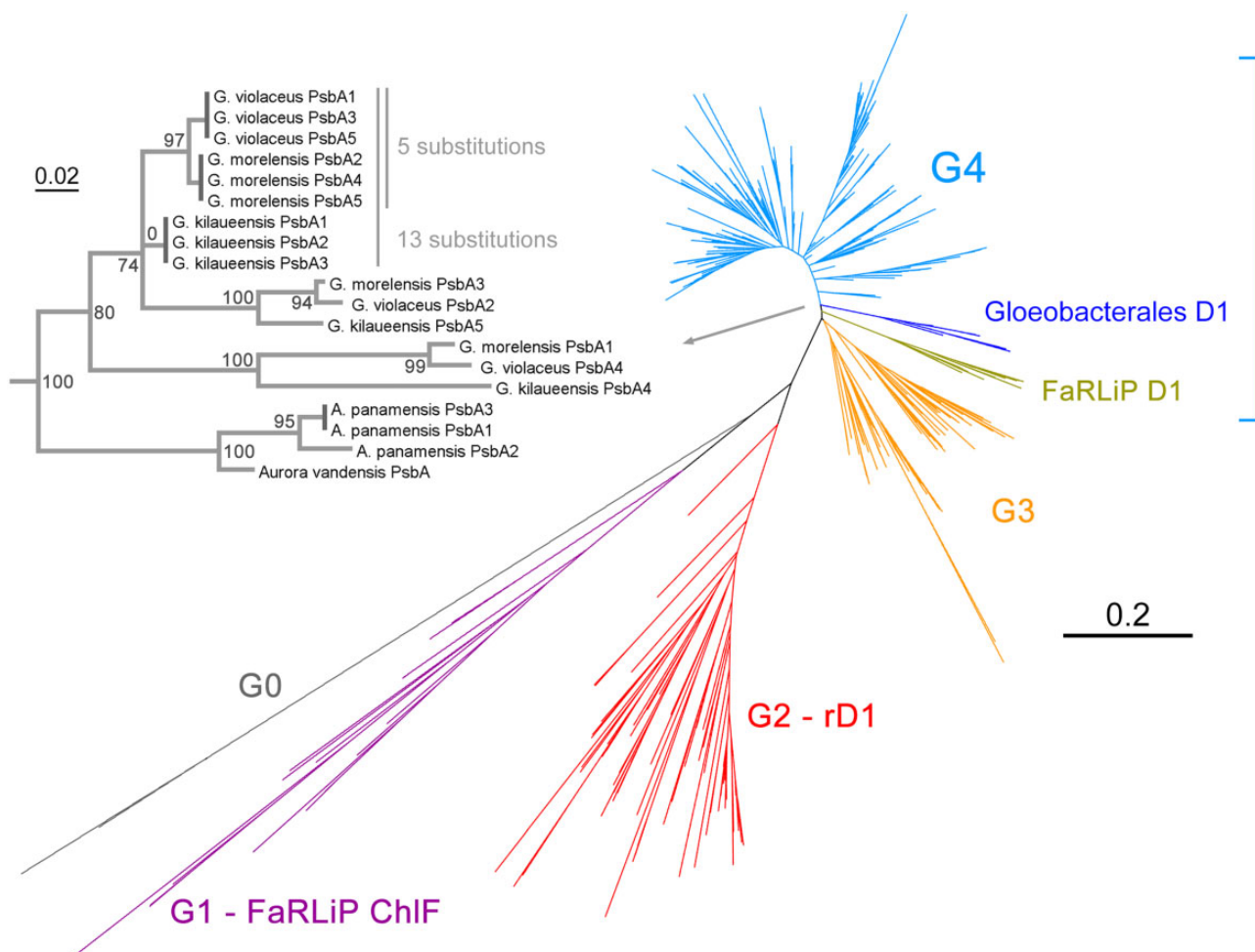


FIG. 2.—Unrooted ML tree of D1 amino acid sequences. Different types of D1 are denoted G0 to G4, representing Group 0 to Group 4 and based on the categorization by Cardona et al. (2015). FaRLiP D1 denotes the standard D1 used in the far-red light acclimation response, whereas FaRLiP ChIF denotes the divergent D1 known to confer “chlorophyll *f* synthase” activity to Photosystem II. Group 2 or rD1 denotes the “rogue” D1, a widespread but atypical form of D1 of unresolved function. The subtree in light gray zooms in on the Group 4 D1 of the Gloeobacterales. The dark gray vertical branches represent intraspecific identical D1 forms (branches of no length). Scale bar denotes amino acid substitutions per site.

sequences known as reported here. These sequences are of unknown function and have accumulated many amino acid substitutions likely to disrupt Photosystem II function if assembled into a complex (Cardona et al. 2015).

The genome of *G. morelensis* encodes six distinct D1 proteins: Three of these were identical to each other, following the same pattern of D1 diversification as the other two *Gloeobacter*. Five of these, the standard D1 (G4) subunits, branched as sister to *G. violaceus* with the sixth being the second atypical Group 0 sequence (fig. 2). The genome of *A. panamensis* encodes three D1 subunits, two of these identical, whereas only one D1 is known for *A. vandensis*. The *Aurora/Anthocerotibacter* sequences clustered as sister to all other *Gloeobacter* standard D1, and thus diverged before the duplication of the main D1 subunits found in the genus *Gloeobacter*. In addition, the tree revealed that the three identical D1 sequences in each of the *Gloeobacter* genomes and

the two identical sequences in *A. panamensis* are in fact distantly related to each other. The three identical sequences in *G. morelensis* compared with the three identical ones in *G. violaceus* differ by five amino acid substitutions, whereas differing by 13 substitutions when compared with that from *G. kilaeensis* and by 52 substitutions when compared with the two identical ones in *A. panamensis*. These patterns suggest not only frequent gene duplications and losses, but also a degree of concerted gene evolution.

Concerted evolution of duplicated genes, in which identical copies evolve as a unit via intragenomic homologous recombination, is known to serve as a molecular mechanism maintaining sequence homogeneity through time of highly similar or identical paralogous genes in both prokaryotes and eukaryotes (Santoyo and Romero 2005). It is plausible that concerted evolution of *psbA* genes (encoding D1), among other factors (Shi et al. 2005), contributed to

Photosystem II maintaining one of the slowest rates of protein evolution since the origin of photosynthesis (Oliver et al. 2021). It is worth noting that this pattern of D1 evolution is not unique to *Gloeobacterales* and similar arrays of identical and variant D1 are found often in other strains of cyanobacteria, including the relatively late emerging heterocystous clade (Cardona et al. 2015). For example, both *Nostoc* sp. PCC 7120 and *Nostoc punctiforme* PCC 73102 each have five standard D1, three of which are also identical in each species, but differing by 25 amino acid substitutions when compared between species. These patterns indicate that this mechanism of photosystem evolution is a feature present since at least the last common ancestor of cyanobacteria.

Conclusion

Our study reports the complete genome sequence of the third *Gloeobacter* species; only two complete genomes had been published thus far in the past 18 years. *Gloeobacter* are considered conditionally rare microbial species that are important and significant to our understanding of the origin and evolution of photosystems in diverse lineages of microbes (Saw 2021). Additional work will be required to further characterize the genes encoded in the plasmids to determine their roles in the ecology of *G. morelensis*. We also found putative molecular evidence for concerted evolution of *psbA* genes (D1) in this lineage, which may have implications for the mechanisms of molecular evolution required for the early diversification of photosystem core proteins before the last common ancestor of cyanobacteria. This study improves our knowledge of *Gloeobacter* species and their genetic diversity, but more genomes are needed to reconstruct a high-resolution view of the origin and evolution of oxygenic photosynthesis.

Materials and Methods

Sample Collection and Cultivation

Samples were collected from a waterfall cave in Morelos, Mexico and brought back to the laboratory of G.M. Samples were grown on BG11 medium as previously described (Montejano et al. 2018). Biofilm sample collection and cultivation were reported in a previous study and pure culture of *G. morelensis* obtained from the biofilm was sent to the laboratory of J.S. at The George Washington University. To obtain enough cells to extract DNA from, the culture obtained from Mexico was restreaked on a BG11 agar plate and the plates were incubated in a light incubator at 28 °C for several weeks until large quantities of cells were visible on the agar plates. DNA was extracted from a single large colony.

Genome Sequencing, Assembly, and Annotation

Genomic DNA of *G. morelensis* was extracted from a single large colony on a quadrant-streaked BG11 agar plate using

Zymo Microbiomics DNA extraction kit and quantified with Qubit 4 fluorometer. Purified genomic DNA was sent to Microbial Genomes Sequencing Center (MiGS) in Pittsburgh, PA. Two separate Illumina samples and one Nanopore sample were obtained from MiGS. Raw sequences were trimmed for quality and contamination using the following tools: bbdutk for Illumina reads and filtlong for Nanopore reads. Trimming parameters for bbdutk were as follows: qtrim=rl trimq=20. Trimming parameters for filtlong were as follows: -min_length 1000 -keep_percent 90 -target_bases 1000000000. Quality-trimmed Illumina and Nanopore sequences were coassembled using Unicycler (v0.4.8) with default parameters. Polishing of the final assembly was done with Pilon, which is integrated in the Unicycler assembler. Circularity of assembled contigs were determined by examining Unicycler assembly paths using the Bandage tool (v0.8.1). Genome completeness and contamination was estimated using CheckM (v1.1.0) (Parks et al. 2015), miComplete (v1.1.1) (Hugoson et al. 2020), and BUSCO (Manni et al. 2021).

Phylogenetic Analysis of D1 Subunits

A total of 1,198 D1 amino acid sequences were retrieved from the NCBI database using BLAST in February 18, 2020. A redundancy cutoff of 98% sequence identity reduced the number of sequences to 540. However, all sequences from all *Gloeobacter* strains, including the identical ones, were kept in the data set. An additional D1 from the metagenome-assembled genome of *A. vandensis* (Grettenberger et al. 2020) and the three amino acid sequences from the genome of *A. panamensis* were later added to the data set (Rahmatpour et al. 2021). Alignments were produced using Clustal Omega (Sievers et al. 2011) using ten combined guided-tree and HMM iterations. Maximum likelihood phylogenetic trees were executed using IQ-TREE 2.0 (Minh et al. 2020), with automatic best model selection, applying ultrafast bootstrap for branch support and run until the bootstrap correlation coefficient of split occurrence frequencies reached a value of 0.99.

Phylogenomic Analysis

PhyloPhlAn version 3.0.51 was used to identify conserved single-copy genes with the following commands: "phylophlan_write_config_file -o custom_phylophlan.ctg -d a -db_aa diamond -map_aa diamond -msa mafft -trim trimal -tree1 fasttree," "phylophlan -f custom_phylophlan.ctg -i faas -proteome_extension .faa -d phylophlan -diversity low -fast -nproc 24 -o phylophlan -t a -verbose 2>&1 | tee log.phylophlan.txt." The resulting concatenated multiple sequence alignment was then used to construct a maximum likelihood phylogenomic tree using IQ-TREE (v2.0.3). The best-fitting model was identified using the command "iqtree -s faas_concatenated.aln -m TESTONLY -T 24 -pre modeltest,"

and the final tree was constructed using the following command “iqtree -s faas_concatenated.aln -m LG+F+G4 -alrt 1000 -bb 1000 -T 24.” Resulting phylogenomic tree was visualized with a custom Python script utilizing the ETE3 Python library (Huerta-Cepas et al. 2016). The script is accessible at the following Github repository: <https://github.com/SawLabGW/Gmor>.

Pangenomic and Comparative Genomic Analyses

Four genomes of *Gloeobacter* (*G. violaceus*, *G. kilaueensis*, *G. morelensis*, *G. SpSt-379*) and two genomes of sister taxa (*A. vandensis* LV9 and *A. panamensis*) were used in this analysis. The accession numbers of the genomes used were: CP062698.1 (*A. panamensis*), JAAXLT010000001.1 (*A. vandensis* LV9), DSQC00000000.1 (*Gloeobacter* SpSt-379), CP003587.1 (*G. kilaueensis* JS1), and BA000045 (*G. violaceus* PCC 7421). *Gloeobacter* SpSt-379 is an incomplete metagenomic bin obtained from a previous study (Zhou et al. 2020). *Aurora vandensis* LV9 and *A. panamensis* genomes were first annotated with Prokka version 1.13 to identify coding regions. These four annotated genomes were analyzed using Anvi'o version 7.0 (Eren et al. 2021) to identify unique and shared gene clusters between them. To perform pangenomic comparisons, “anvi-pan-genome” command was used with default parameters. ANIs between the strains were calculated with the “anvi-compute-genome-similarity” command with “-program pyANI” option. Complete list of commands and workflow used in this analysis are documented in a Markdown file deposited to a Github repository (<https://github.com/SawLabGW/Gmor>).

Supplementary Material

Supplementary data are available at *Genome Biology and Evolution* online.

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Data Availability

The complete genome sequence of *Gloeobacter morelensis* has been deposited to GenBank under accession numbers CP063845–CP063847. Raw Illumina and Nanopore

sequences have been deposited to NCBI Sequence Reads Archive (SRA) under accession numbers SRR12931218 and SRR12931219, respectively.

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